

WHY STUDY BIOINFORMATICS AT DYPU?

Bioinformatics is an interdisciplinary science where tools of information technology are used to process and analyze biological data which are otherwise hard to do using conventional ways. Often the data generated by Molecular Biologists and Biochemists may be very huge like DNA sequence data or proteomic data which may run to many pages and may not make sense to our naked eyes and intellect. Here we may have to take the help of computers, software programs or in one sentence the help of Bioinformatics. Even though many software programs are available in the public domain, often trained Bioinformatics specialists are not available easily. There is a need for more trained man/woman power in this field to cater to the needs of research and development, pharmaceutical industry, medicine and agriculture. The persons need to be familiar with Molecular Biology, Biochemistry as well as computers. Even though Bioinformatics programs are run by various institutions, there is still lack of good Bioinformatics specialists. Department of Biotechnology (DBT), New Delhi (Government of India), has significantly contributed to the development of human resources in Bioinformatics in our country through their Biotechnology information network system. The PG diploma in Bioinformatics offered by DYPU, Department of SCRM and MBT, under the Center for Interdisciplinary studies is intended to create quality human resources in Bioinformatics. This will be an add on course to MSc and may empower the students to gain meaningful employment in this emerging field of study contributing to agriculture, medicine and pharmaceutical sciences and industry. In addition to under graduates as well as graduate students in basic sciences, it will be very much useful to medical and pharmacy graduates by facilitating their access to the future opportunities in research and development. We welcome you to this exciting opportunity to learn Bioinformatics with us at DYPU!

D. Y. PATIL EDUCATION SOCIETY, KOLHAPUR (DEEMED TO BE UNIVERSITY). *Re-accredited by NAAC with 'A' Grade.* Centre for Interdisciplinary Research, , India. Department of Stem Cell & Regenerative Medicine and Medical Biotechnology.869, 'E', D.Y. Patil Vidyanagar, Kasaba Bavada, Kolhapur-416006(MS).Maharashtra. India.

POSTGRADUATE DIPLOMA IN BIOINFORMATICS (PGDB)

DURATION: One year

PATTERN: Semester

NUMBER OF SEATS: 10

FEES: Rs. 25,000 (To be paid in two installments). Exam fees and other fees will be applicable as per
ADMISSION: First come first served.

ELIGIBILITY : Any recognized BSc degree in Science with Biology background, MBBS, BAMS, BHMS, BUMS, BPHARM, BVSC. MSc final year students, PhD students and Faculty members of SCRM, CIR, DYPU, and Kolhapur are encouraged to apply

SPECIAL OFFER: For this year (2019) only. Fees will be Rs. 10,000 for faculty members and PhD students of DYPU (to be paid in two installments)

COURSE STRUCTURE:

THEORY PAPERS

PGDB 1: FUNDAMENTALS OF BIOLOGICAL SCIENCES: 4 Credits

PGDB 2: INTRODUCTION TO COMPUTERS: 4 Credits

PGDB 3: GENOMICS AND PROTEOMICS: 4 Credits

PGDB 4: COMPUTATIONAL METHODS AND DRUG DISCOVERY: 4 Credits

PRACTICALS AND RESEARCH PROJECT WORK

PGDBP 1(.Practicals): 4 Credits

PGDBP 2.(Practical) : 2 Credits

PGDBP 3 (Research Project): 2 Credits

TOTAL: 24 Credits

REQUIREMENTS:

Computer Lab with minimum twenty computers with soft wares

Class room: Two

Printer

ASSISTANT PROFESSORS

PhD IN BIOLOGICAL SCIENCE WITH EXPERTISE IN BIOINFORMATICS AND COMPUTER SCIENCE.

One person with bioinformatics background, one person with Computer sciences with expertise in soft wares

SCHEME OF EXAMINATION:

Examinations will be at the end each semester

THEORY: PGDB 1: FUNDAMENTALS OF BIOLOGICAL SCIENCES

THEORY PGDB 2: INTRODUCTION TO COMPUTERS

THEORY PGDB 3: GENOMICS AND PROTEOMICS

THEORY PGDB 4: COMPUTATIONAL METHODS AND DRUG DISCOVERY

PGDBP 1 (PRACTICALS)

PGDBP 2(PRACTICALS):

PGDBP 3 (RESEARCH PROJECT)

TOTAL: 24 Credits.

Theory papers External: 3 Credits. Internal: 1 Credits. Total 4 Credits

Practical One. . External 3 Credits. Internal: 1 Credits. Total 100 marks

Practical two: 2 Credits (1.5 Credits external. 0.5 Credits internal Total 2 Credits

Project work: 2 Credits (1.5 Credits external. 0.5 Credits internal. . Total 2 Credits

THEORY EXAMINATION PATTERN: Descriptive, MCQ, problem solving.

PROJECT WORK: Original bioinformatics research, Submission of project report and presentation of work and open defense in front of external and internal examiners. Research projects will be assigned at the beginning of the Course. .Soft as well as the bound copy of the project report need to be submitted to the guide for evaluation and Certification well in advance of the Presentation. The project work will be subjected to plagiarism check.

TEACHING AND TRAINING: Training will involve class room teaching by in house experts, invited experts, Seminars, home work Assignments, practical sessions, discussions, problem solving sessions and research project.

COUNSELING SESSIONS: Counseling sessions will be held on Saturdays except 2 and 4 Saturday and National holidays.

PGDB Course : Time Table and Work Load Distribution

Work Load: 11 HRS per week.

Requirement :One Full time Assistant Professor.

One Full Time computer specialist

Proposed Time Table:

Semester I

Day	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
Time						
11.00am-12.00pm	Paper I	Paper I	Paper I	Paper I	PRACTICAL	SEMINAR
12.00pm-1.00pm	Paper II	Paper II	Paper II	Paper II	PRACTICAL	SEMINAR
1.00am-2.00pm	Research project	Research project	Research project	Assessment (PH)	PRACTICAL	SEMINAR

Semester II

Day	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
Time						
11.00am-12.00pm	Paper III	Paper III	Paper III	Paper III	PRACTICAL	SEMINAR
12.00pm-1.00pm	Paper IV	Paper IV	Paper IV	Paper IV	PRACTICAL	SEMINAR
1.00am-2.00pm	Research project -	Research project -	Research project -	Assessment (PH)	PRACTICAL	SEMINAR

SYLLABUS OF PG DIPLOMA IN BIOINFORMATICS (PGDB).July 2019

- **One Year Diploma Course**
- **Semester System following Choice Based Credit System**
- **Total Credits =24 Credits**

Semester I (Total Credits -12)

Theory Paper I (PGDB 1): Fundamentals Of Biological Sciences: 4 Credits

Theory Paper II (PGDB 2): Introduction To Computers: 4 Credits

Practical I (PGDBP 1): 4 Credits

Semester II (Total Credits -12)

Theory Paper III (PGDB 3): Genomics And Proteomics: 4 Credits

Theory Paper IV (PGDB 4): Computational Methods And Drug Discovery: 4 Credits

Practical II (PGDBP 2): 2 Credits

Dissertation Project (PGDBP 3) : 2 Credits

Semester I

Theory Paper I (PGDB 1): Fundamentals Of Biological Sciences: 4 Credits

Hours:60 Hrs

UNIT I (15)

A) PROTEINS:

General properties and structures of amino acids, Classification of proteins; based on shape, size, functions (Enzyme, transport, storage, contractile, structural, defense and regulatory). secondary structures of proteins, tertiary and quaternary structures of proteins, Peptide bond, restriction rotation, Ramchandran Plot, Protein folding classes, studying primary structure of protein, protein conformation prediction, Protein degradation

B) NUCLEIC ACIDS:

Structure of nucleoside, nucleotide. Nucleotide synthesis pathways. Secondary structure of DNA, Watson and Crick model of DNA. Forms of DNA: A, B and Z, Degradation of nucleic acids.

UNIT II (15)

A) CARBOHYDRATES:

Classification, characteristics and functions monosaccharides, disaccharides, polysaccharides, Epimers, Isomers, Anomers, Chiral carbon atom, chair and boat conformation, glucopyranose and fructopyranose, Carbohydrate metabolism pathways: glycolysis, gluconeogenesis, glycogenolysis, glycopyranose, fructopyranose.

B) LIPIDS: Definition and classification of lipids, fatty acids, general formula, nomenclature and chemical properties, structure function and properties of simple, complex, acylglycerols, phosphoglycerides, waxes, terpins, steroids and postaglands.

UNIT III (15)

ENZYMES:

Enzymes Classification, IUB system, Enzyme structure, active site of enzymes, enzyme substrate complex formation, Rate of enzymatic reaction, effects of various parameters on

enzymatic reaction, activation energy, transition state theory, enzyme activity, enzyme assay, Derivation of Michaelis-Menten(K_m) equation, Significance and applications of V_{max} and K_m , enzyme inhibition, Different types of inhibitors, Structure and function of enzymes eg. Chymotrypsin, trypsin, elastase, $Na^+ K^+$ ATPase, enzyme regulation.

UNIT IV

(15)

CELL ORGANELLES:

Cell as a basic unit of life, prokaryotic and eukaryotic cells, structural and functional different cell organelles; cell membrane, cell wall, nucleus, mitochondria, chloroplast, lysosomes, protein translocation in golgi bodies and ER.

REFERENCES

1. Lehninger, A. L., Nelson, D. L., & Cox, M. M. (2000). Lehninger Principles of Biochemistry. New York: Worth Publishers. USA.
2. Lodish, H. F. (2013). Molecular Cell Biology. New York: W.H. Freeman and Co. USA
3. Loewy and Gallant. (1991) Cell Structure and Function, Thomson Learning USA,
4. Berg, J. M., Tymoczko, J. L., Stryer, L., & Stryer, L. (2002). Biochemistry. New York: W.H. Freeman. USA
5. Price and Steavenson (2000) Fundamentals of Enzymology, Oxford, United Kingdom
6. Shulz and Schimer (1979) Principles of Protein Structure New York, USA

Theory Paper II (PGDB 2): Introduction To Computers: 4 Credits

Hours:60 Hrs

UNIT I

(15)

A) BASIC OF COMPUTER: Computer history; Computer generations, Computer classifications, analog, digital, miniframe, mainframe, micro computers, fundamentals of logical concepts.

Digital computers: basic operation of digital computers, structure of digital computers; arithmetic unit, central unit, memory unit, Input unit and output unit.

B) COMPUTER CODING: Number system, binary number system, decimal number system, binary to decimal conversion, Binary arithmetic, octal number system, hexadecimal number system.

UNIT II

(15)

A) COMPUTER LANGUAGES: Machine level languages, assembly level languages, high level languages

B) INPUT OUTPUT AND MEMORY DEVICES: paper tape, Punched card reader, reader, magnetic tape, floppy disk, magnetic disk, optical scanner, voice data, entry terminal, teleprocessing terminal, visual display unit, modern input devices, Output devices; CRT, plotter, printer,

C) MEMORY: RAM, ROM, PROM, EPROM, EEPROM, Primary memory or main memory; magnetic core memory, semi-conductor memory, Secondary memory or auxillary memory or storage devices; Hard disk, discket, ZIP, devices, digital tape, CD-ROM, DVD, virtual, memory, cache memory.

UNIT III

(15)

A) OPERATING SYSTEMS: Mac OS, UNIX/LINUX, DOS, windows 98/XP/VISTA, VMS.

B) MODERN COMPUTERS: Parallel processing computers, Workstations, Super-computers.

C) INTERNET AND RELATED PROGRAMMES: World Wide Web, HTML, HTTP, telnet, FTP, computer domain.

D) BIOSTATISTICS: Mean, median, mode, comparison between mean median and mode, measures of dispersion: range, variation, standard deviation, coefficient of variation, symmetry, probability distribution. Bar diagram, histogram. Pie diagram, cumulative frequency curves.

UNIT IV

(15)

A) MATHEMATICS: 1) SETS: Finite set, infinite set, null or void set, subset, Intervals; closed and open, universal set, operations of set. Relations and functions.

2) MATRICES: Types of matrices, properties of matrices, addition, subtraction of matrices, matrix, multiplication, elementary transformation, inverse of matrices. DETERMINANTS: Definition, properties associated with determinants. Trigonometry and Derivatives.

B) DATABASES: Concept of data, data mining, data models, data representation, various types of databases, biological data and data analysis. Related programs; Oracle, VB, SQL, Database management System (DBMS). Introduction to protein and nucleic acid databases.

REFERENCES

1. T. Bhaskara Rao.(2004) Methods of Biostatistics, Hyderabad : Paras Medical Publisher,INDIA
2. Cynthia Gibas and Per Jambeck (2001)Developing Bioinformatics Computer Skills. O'Reilly Media, Inc USA,
3. J. M. Martin, Prentice-Hall(2008) Introduction to database system., Prentice Hall Press, USA

PGDBP 1 (PRACTICALS)

1. Computer basic knowledge.
2. Internet surfing and searching information, downloading and installing software (Acrobat Reader, etc)..
3. Hands on session with basic Microsoft Word, Microsoft Excel, Microsoft Access etc.
4. Creation of computer presentation with MS Power Point.
5. Introduction to Oracle for creation of database.
6. Learning C language.
7. Literature database introduction at NCBI, PUBMED.
8. Retrieval of the amino acid sequences from protein sequence database.
9. Extraction of gene sequences by from nucleic acid databases.
10. Visualization of 3-D structure of protein and measurement of bond length, bond angle and torsion angles using RasMol.
11. Secondary and tertiary structural analysis of protein.

Semester II

Theory Paper III (PGDB 3): Genomics And Proteomics: 4 Credits
Hours:60 Hrs

UNIT I (15)

A) GENOMICS: Human Genome Project, cloning vectors, concept of maps, physical maps, shotgun libraries, DNA polymorphism, DNA sequences.

B) SEQUENCE DATABASES: GeneBank, EMBL Nucleotide sequence databank, DDBJ, database annotations. Recombinant DNA technology, restriction enzymes, resource for restriction enzyme (REBASE), Similarity and conformational search.PCR, primer selection for PCR, BLASTn, application of BioEdit.

C) GENE IDENTIFICATION:Genome information and special features, cDNA library,coding sequences, untranslated regions, expressed sequence tags, Approach to gene identification; masking repetitive DNA, database search, codon-bias detection, detecting functional sites in the DNA. Internet resources for gene identification, functional sitesdetection, gene expression.

UNIT II (15)

A) GENE EXPRESION AND MICROARRAY CONCEPT

Introduction of gene expression, Microarrays basic concept; Types of arrays: spotted, oligonucleotide, Microarray experiment design, Clustering gene expression profiles, Tools for microarray analysis; soft-finder, xCluster, MADAM, SAGE, Microarray design, microarray experimentation, fabrication computational analysis of Microarray data. Microarry applications.

UNIT III (15)

PROTEOMICS: Protein sequence information, composition and properties, physicochemical properties based on protein sequence, sequence comparison, Sequence analysis, Primary databases, Secondary, databascs. Sequence alignment: Pairwise, multiple, local, global sequence alignment, Scoring matrices:PAM250, BLOSUM62, Sequence alignment programs: ClustalW, BioEdit, BLASTp

UNIT IV (15)

A) TOOLS AND TECHNIQUES IN PROTEOMICS:affinity chromatography,gel filtration,HPLC,ICAT,PAGE, 2-D gel electrophoresis, isoelectric focusing, Mass spectroscopy for protein analysis, Tandem mass spectroscopy (MS/MS),tryptic digestion and peptide fingerprinting (PMF), MALDI-TOF, Electrospray ionization, analysis, Protein Micro array in protein expression, profiling and diagnostics, drug target identification. Database searching, Three dimensional structure determination:X-ray, NMR.

B) PHYLOGENETIC ANALYSIS:Evolution concept, elements of phylogeny, methods of phylogenetic analysis, comparison of genetic sequence of organisms, phylogenetic analysis tools-Phylip, ClustalW, Use of different Softwares: MEGA4, Phylip, BLAST.

REFERENCES

1. C. Stain Tsai (2002)An introduction to Computational Biochemistry . New York, , A. John Wiley and Sons, Inc., Publications. USA
2. Rastogi, S. C., Mendiratta and Rastogi, P (2013) Bioinformatics; Methods and applications; Genomics, Proteomics and Drug Discovery;New Delhi India, PHI Learning Pvt. Ltd. USA
3. Atwood, T. K. and Parry-Smith, D. J Introduction to Bioinformatics, (2002).China, Peking University Press,China.
4. Bioinformatics; A practical guide to the analysis of genes and proteins.; Edited by, Andreas D. Baxevanis and Francis Oulelette. (2005) Hoboken, N.J. : Wiley. USA

Theory Paper IV (PGDB 4): Computational Methods And Drug Discovery: 4 Credits
Hours:60 Hrs

UNIT I (15)

A) BIOLOGICAL STRUCTURES:

structures of Nucleic acid, various ribose ring conformations, ribose-ring puckering, conformational study, DNA-binding proteins, RNA-binding proteins, protein-protein interactions, protein-ligand interactions, Ramachandran plot, Biophysical aspects of proteins and nucleic acids.

B) DATABASES; Protein Data bank, Nucleic Acid Data Bank, Molecular modeling Data Bank. Prediction of Secondary structure, three-dimensional structure, protein folding and functional sites, protein folding classes.

UNIT II (15)

PROTEIN STRUCTURE PREDICTION; prediction of protein structure from sequences, Homology modeling, functional sites, Protein folding problem, protein folding classes, Protein identification and characterization; TagIdent, AACompIdent, PepIdent, MultiIdent; PROSEARCH, PepSea, PepMAPPER, FindPept, Predicting transmembrane helices, Primary structure and Secondary structure analysis and prediction, motifs, profiles, patterns and fingerprints search. Methods of sequence based protein prediction.

UNIT III (15)

MOLECULAR MODELING: Introduction to MM, force field, quantum chemistry, Schrödinger equation, potential energy functions, energy minimization, local and global minima, saddle point, grid search, various approximations: LCAO, HF, semi-empirical calculations; single point calculations, full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1, conformational search, Z-matrix, Molecular docking, Molecular modeling packages.

MOLECULAR MECHANICS CONCEPTS: Definition, balls and springs, force fields, bond-stretching, bond-bending, dihedral motions, out of plane angle potential, non-bonded interaction, coulomb interactions, conformational search, united atoms and cut-offs, Derivative methods; First-order methods;

ENERGY MINIMIZATION METHODS: Steepest descent, conjugate gradient, Second order methods; Newton-Raphson method.

UNIT IV

(15)

MOLECULAR DYNAMIC SIMULATIONS: Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, Molecular dynamics methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, MDrun duration. Analysis of structures before and after MD, uses in drug designing, Finding ligand protein interactions.

DRUG DISCOVERY: Introduction, drug discovery area, Applications of drug discovery, parameters in drug discovery, identification of drug target molecules, Approaches of drug design, computer-aided drug designing methods; computer aided molecular design (CAMD), Quantum CAChe and project leader, ligand design methods, docking programs.

REFERENCES

1. Rastogi, S. C. and Mendiratta and Rastogi, P (2013) Bioinformatics; Methods and applications; Genomics, Proteomics and Drug Discovery;, PHI Learning Pvt. Ltd. New Delhi India
2. Cynthia Gibas and Per Jambeck (2001) Developing Bioinformatics Computer Skills. O'Reilly Media, Inc. USA,
3. C. Stain Tsai (2002)An introduction to Computational Biochemistry New York . John Wiley and Sons, Inc., Publications. USA.

PGDBP 2 (PRACTICALS):

1. Basic UNIX commands, pine, telnet, ftp.
2. RasMol command line for structural analysis.
3. Investigation of molecular interactions using the program CHIMERA.
4. BLAST program for Similarity search.
5. Pair-wise and multiple sequence sequence alignment by using ClustalW.
6. Alignment editing using BioEdit.

7. Phylogenetic analysis using online tools.
8. Homology Modeling using SPDBV.
9. Molecular modeling using SPARTAN.
10. Energy minimization using software.
11. Molecular dynamics simulation using GROMACS etc.
12. Analysis of structure after Molecular Docking using CHIMERA.

PGDBP 3 (RESEARCH PROJECT WORK)

TO BE SUBMITTED AT THE END OF THE YEAR